

Clone 40:

GAATTCGGCACCAGTTCGGAAAAGAACAAAATGGCTTGTATCGTTTTTCGTT
GCTCTTGTGCTCTATGCTTAATGCAACCGGGTTCGGGTGAGGAAGTACA
ATGCGCGATGAATTGGACACAAGCTAATGAATATGTGTTCAACGTGGACT
GGATGACCATTTTCATCTACGACTATGGCGCTCAAGAGCAACTGTACGAA
GATCGGGCTTTGGGGCTGTGTCTGGATTGAACGGGCCGGCCAGGTACCCAC
AAAAGCCGTCTGGATTAACTGGAGTAACGACACGCAGTCATGTGTAACAA
GAAAAACAATCTTCTTCGAGGTGGTGGAGAAATTGCCCGGCTAGTTGAC
TACAGACCACAGGAAGACGGAACTGAGAAAACCTTTTACAAGAAAATTCTC
TAGCAAAATGCCAGGCACCTACATGCTTATGGACGTGTGCGCTACAAGGG
ACGCTGATGATAAATGCATCGAAGGCACAATTGTGGTGACAGTCAGGGTG
TCCCTATATGACGAAGATAACAATGGTGTAAATGGATGAAGGTAAGGTGAT
TCCATCTGAGACAATCGAGGATGATATCAAGGACTGTGGGCTCTTAGACC
AAGATGTTGAACTCGATTATACGTGGACTCAAAACGAGTGTGATCTACCA
GACACAGTAGACGAGGCTGAAGACACACCGTCAGAACTGGAGAATTCTT
CTGGTAGATCTATCAGACTACTTTTATCAGCAGGACAACCTGGTCGTTACC
AGACACCTATAACGTGTCTCTCATCAATAATGTGTAACAGAAATAATCG
ATAGAATATTGAAAATAAAATGTTAATAAACACTGGTTGAAATATGAAAA
AAAAAAAAAAAAAACTCGAG

Clone 3:

GAATTCGGCACCAGGGAAAAGAACAAAATGGCTTGTATCGTTTTTCGTT
GCTCTTGTGCTCTATGCTTAATGCAACCGGGTTCGGGTGAGGAAGTACA
ATGCGCGATGAATTGGACACAAGCTAATGAATATGTGTTCAACGTGGACT
GGATGACCATTTTCATCTACGACTATGGCGCTCAAGAGCAACTGTACGAG
GATCGGGCTTTGGGGCTGTGTCTGGATTGAACGGGCCGGCCAGGTACCCAC
AAAAGCCGTCTGGATTAACTGGAGTAACGACACGCAGTCATGTGTAACAA
GAAAAACAATCTTCTTCGAGGTGGTGGAGAAATTGCCCGGCTAGTTGAC
TACAGACCACAGGAAGACGGAACTGAGAAAACCTTTTACAAGAAAATTCTC
TAGCAAAATGCCAGGCACCTACATGCTTATGGACGTGTGCGCTACAAGGG
ACGCTGATGATAAATGCATCGAAGGCACAATTGTGGTGACAGTCAGGGTG
TCCCTATATGACGAAGATAACAATGGTGTAAATGGATGAAGGTAAGGTTAT
TCCATCTGAGACAATCGAGGATGATATCAAGGACTGTGGGCTCTTAGACC
AAGATGTTGAACTCGATTATACGTGGACTCAAAACGAGTGTGATCTACCA
GACACAGTAGACGAGGCTGAAGACACACCGTCAGAACTGGAGAATTCTT
CTGGTAGATCTATCAGACCCTTTTATCAGCAGGACAACCTGGTCGTTACC
AGACACCTATAACGTGTCTCTCATCAATAATGTGTAACAGAAATAATCG
ATAGAATATTGAAAATAA

Clone 5:

GTCCGAAAAGAACAAAATGGCTTGTATCGTTTTTCGTTGCTCTTGTGCTCTATGCTTAATGCAACCGGG
TTCCGGTGAGGAAGTACAATGCGCGATGAATTGGACACAAGCTAATGAATATGTGTTCAACGTGGACTG
GATGACCATTTTCATCTACGACTATGGCGCTCAAGAGCAACTGTACGAGGATCGGGCTTTGGGGCTGTG
TCGGATTGAACGGGCCGGCCAGGTACCCACAAAAGCCGTCTGGATTAACTGGAGTAACGACACGCAGTC
ATGTGTAACAAGAAAAACAATCTTCTTCGAGGTGGTGGAGAAATTGCCCGGCTAGTTGACTACAGACC
ACAGGAAGACGGAACTGAGAAAACCTTTTACAAGAAAATTCTCTAGCAAAATGCCAGGCACCTACATGCT
TATGGACGTGTGCGCTACAAGGGACGCTGATGATAAATGCATCGAAGGCACAATTGTGGTGACAGTCAG
GGTGTCCCTATATGACGAAGATAACAATGGTGTAAATGGATGAAGGTAAGGTTATTCCATCTGAGACAAT
CGAGGATGATATCAAGGACTGTGGGCTCTTAGACCAAGATGTTGAACTCGATTATACGTGGACTCAAAA
CGAGTGTGATCTACCAGACACAGTAGACGAGGCTGAAGACACACCGTCAGAACTGGAGAATTCTTCTG
GTAGATCTATCAGACCCTTTTATCAGCAGGACAACCTGGTCGTTACCAGACCTATAACGTGTCTCTCA
TCAATAATGTGTAACAGAAATAATCGATAGAATATTGAAAATAAAATGTTAATAGACACTGGTTGAA
AAAAAAAAAAAAAACTCGAG

Fig. 1

clone 40 GAATTCGGCAGGAGTCGGAAAAGAACAAAATGGCTTGTATCGTTTTCGTT
clone 3 GAATTCGGCAGGAG--GGAAAAGAACAAAATGGCTTGTATCGTTTTCGTT
clone 5 -----GTCGGAAAAGAACAAAATGGCTTGTATCGTTTTCGTT
* * * * *

clone 40 GCTCTTGTGCGCTCTATGCTTAATGCAACCGGGTTCCGGTGAGGAAGTACA
clone 3 GCTCTTGTGCGCTCTATGCTTAATGCAACCGGGTTCCGGTGAGGAAGTACA
clone 5 GCTCTTGTGCGCTCTATGCTTAATGCAACCGGGTTCCGGTGAGGAAGTACA
* * * * *

clone 40 ATGCGCGATGAATTGGACACAAGCTAATGAATATGTGTTCAACGTGGACT
clone 3 ATGCGCGATGAATTGGACACAAGCTAATGAATATGTGTTCAACGTGGACT
clone 5 ATGCGCGATGAATTGGACACAAGCTAATGAATATGTGTTCAACGTGGACT
* * * * *

clone 40 GGATGACCATTTCATCTACGACTATGGCGCTCAAGAGCAACTGTACGAA
clone 3 GGATGACCATTTCATCTACGACTATGGCGCTCAAGAGCAACTGTACGAG
clone 5 GGATGACCATTTCATCTACGACTATGGCGCTCAAGAGCAACTGTACGAG
* * * * *

clone 40 GATCGGGCTTTGGGGCTGTGTGCGGATTGAACGGGCCGGCCAGGTACCAC
clone 3 GATCGGGCTTTGGGGCTGTGTGCGGATTGAACGGGCCGGCCAGGTACCAC
clone 5 GATCGGGCTTTGGGGCTGTGTGCGGATTGAACGGGCCGGCCAGGTACCAC
* * * * *

clone 40 AAAAGCCGTCTGGATTAAGTGGAGTAACGACACGCAGTCATGTGTAACAA
clone 3 AAAAGCCGTCTGGATTAAGTGGAGTAACGACACGCAGTCATGTGTAACAA
clone 5 AAAAGCCGTCTGGATTAAGTGGAGTAACGACACGCAGTCATGTGTAACAA
* * * * *

clone 40 GAAAAACAATCTTCTTCGAGGTTGGTGGAGAAATTGCCCGGCTAGTTGAC
clone 3 GAAAAACAATCTTCTTCGAGGTTGGTGGAGAAATTGCCCGGCTAGTTGAC
clone 5 GAAAAACAATCTTCTTCGAGGTTGGTGGAGAAATTGCCCGGCTAGTTGAC
* * * * *

clone 40 TACAGACCACAGGAAGACGGAAGTGAAGAACTTTTACAAGAAATTCCTC
clone 3 TACAGACCACAGGAAGACGGAAGTGAAGAACTTTTACAAGAAATTCCTC
clone 5 TACAGACCACAGGAAGACGGAAGTGAAGAACTTTTACAAGAAATTCCTC
* * * * *

clone 40 TAGCAAAATGCCAGGCACCTTACATGCTTATGGACGTGTGCGCTACAAGGG
clone 3 TAGCAAAATGCCAGGCACCTTACATGCTTATGGACGTGTGCGCTACAAGGG
clone 5 TAGCAAAATGCCAGGCACCTTACATGCTTATGGACGTGTGCGCTACAAGGG
* * * * *

clone 40 ACGCTGATGATAAATGCATCGAAGGCACAATTGTGGTGACAGTCAGGGTG
clone 3 ACGCTGATGATAAATGCATCGAAGGCACAATTGTGGTGACAGTCAGGGTG
clone 5 ACGCTGATGATAAATGCATCGAAGGCACAATTGTGGTGACAGTCAGGGTG
* * * * *

clone 40 TCCCTATATGACGAAGATAACAATGGTGTAATGGATGAAGGTAAGGTGAT
clone 3 TCCCTATATGACGAAGATAACAATGGTGTAATGGATGAAGGTAAGGTGAT
clone 5 TCCCTATATGACGAAGATAACAATGGTGTAATGGATGAAGGTAAGGTGAT
* * * * *

clone 40 TCCATCTGAGACAATCGAGGATGATATCAAGGACTGTGGGCTCTTAGACC
clone 3 TCCATCTGAGACAATCGAGGATGATATCAAGGACTGTGGGCTCTTAGACC
clone 5 TCCATCTGAGACAATCGAGGATGATATCAAGGACTGTGGGCTCTTAGACC
* * * * *

Fig. 2 (Part 1 of 2)

clone 40 AAGATGTTGAACTCGATTATACGTGGACTCAAAACGAGTGTGATCTACCA
clone 3 AAGATGTTGAACTCGATTATACGTGGACTCAAAACGAGTGTGATCTACCA
clone 5 AAGATGTTGAACTCGATTATACGTGGACTCAAAACGAGTGTGATCTACCA

clone 40 GACACAGTAGACGAGGCTGAAGACACACCGTCAGAACTGGAGAATTCTT
clone 3 GACACAGTAGACGAGGCTGAAGACACACCGTCAGAACTGGAGAATTCTT
clone 5 GACACAGTAGACGAGGCTGAAGACACACCGTCAGAACTGGAGAATTCTT

clone 40 CTGGTAGATCTATCAGACTACTTTTATCAGCAGGACAACCTGGTCGTTACC
clone 3 CTGGTAGATCTATCAGACCACCTTTTATCAGCAGGACAACCTGGTCGTTACC
clone 5 CTGGTAGATCTATCAGACCACCTTTTATCAGCAGGACAACCTGGTCGTTACC

clone 40 AGACACCTATAACGTGTCCTCATCAATAATGTGTAAAACAGAAATAATCG
clone 3 AGACACCTATAACGTGTCCTCATCAATAATGTGTAAAACAGAAATAATCG
clone 5 AGACACCTATAACGTGTCCTCATCAATAATGTGTAAAACAGAAATAATCG

clone 40 ATAGAATATTGAAAATAAAATGTTAATAAACACTGGTTGAAATATGAAAA
clone 3 ATAGAATATTGAAAATAA-----
clone 5 ATAGAATATTGAAAATAAAATGTTAATAGACACTGGTTGAAA-----AAA

clone 40 AAAAAAAAAAAAACTCGAG
clone 3 -----
clone 5 AAAAAAAAAAAAACTCGAG

Fig. 2 (Part 2 of 2)

Untranslated region

GAATTTCGGGCACGAGTCGGAAAAGAACAAA

Translated region

ATG GCT TGT ATC GTT TTC GTT GCT CTT GTC GCT CTA TGC TTA ATG	45
M A C I V F V A L V A L C L M	
CAA CCG GGT TCC GGT GAG GAA GTA CAA TGC GCG ATG AAT TGG ACA	90
Q P G S G E E V Q C A M N W T	
CAA GCT AAT GAA TAT GTG TTC AAC GTG GAC TGG ATG ACC ATT TTC	135
Q A N E Y V F N V D W M T I F	
ATC TAC GAC TAT GGC GCT CAA GAG CAA CTG TAC GAA GAT CGG GCT	180
I Y D Y G A Q E Q L Y E D R A	
TTG GGG CTG TGT CGG ATT GAA CGG GCC GGC CCA GGT ACC ACA AAA	225
L G L C R I E R A G P G T T K	
GCC GTC TGG ATT AAC TGG AGT AAC GAC ACG CAG TCA TGT GTA ACA	270
A V W I N W S N D T Q S C V T	
AGA AAA ACA ATC TTC TTC GAG GTT GGT GGA GAA ATT GCC CGG CTA	315
R K T I F F E V G G E I A R L	
GTT GAC TAC AGA CCA CAG GAA GAC GGA ACT GAG AAA ACT TTT ACA	360
V D Y R P Q E D G T E K T F T	
AGA AAA TTC TCT AGC AAA ATG CCA GGC ACT TAC ATG CTT ATG GAC	405
R K F S S K M P G T Y M L M D	
GTG TGC GCT ACA AGG GAC GCT GAT GAT AAA TGC ATC GAA GGC ACA	450
V C A T R D A D D K C I E G T	
ATT GTG GTG ACA GTC AGG GTG TCC CTA TAT GAC GAA GAT AAC AAT	495
I V V T V R V S L Y D E D N N	
GGT GTA ATG GAT GAA GGT AAG GTG ATT CCA TCT GAG ACA ATC GAG	540
G V M D E G K V I P S E T I E	
GAT GAT ATC AAG GAC TGT GGG CTC TTA GAC CAA GAT GTT GAA CTC	585
D D I K D C G L L D Q D V E L	
GAT TAT ACG TGG ACT CAA AAC GAG TGT GAT CTA CCA GAC ACA GTA	630
D Y T W T Q N E C D L P D T V	
GAC GAG GCT GAA GAC ACA CCG TCA GAA ACT GGA GAA TTC TTC TGG	675
D E A E D T P S E T G E F F W	
TAG ATC TAT CAG ACT ACT TTT ATC AGC AGG ACA ACT GGT CGT TAC	720
*	
CAG ACA CCT ATA ACG TGT CCT CAT CAA TAA	750

* = stop for translation

Fig. 4A

SUBSTITUTE SHEET (RULE 26)

T000000-2477E800

EcoR I

GAATTCGGCACGAGTCGGAAAAGAACAAA

ATG GCT TGT ATC GTT TTC GTT GCT CTT GTC GCT CTA
TGC TTA ATG CAA CCG GGT TCC GGT GAG GAA GTA CAA
TGC GCG ATG AAT TGG ACA CAA GCT AAT GAA TAT GTG
TTC AAC GTG GAC TGG ATG ACC ATT TTC ATC TAC GAC
TAT GGC GCT CAA GAG CAA CTG TAC GAA GAT CGG GCT
TTG GGG CTG TGT CGG ATT GAA CGG GCC GGC CCA GGT
ACC ACA AAA GCC GTC TGG ATT AAC TGG AGT AAC GAC
ACG CAG TCA TGT GTA ACA AGA AAA ACA ATC TTC TTC
GAG GTT GGT GGA GAA ATT GCC CGG CTA GTT GAC TAC
AGA CCA CAG GAA GAC GGA ACT GAG AAA ACT TTT ACA
AGA AAA TTC TCT AGC AAA ATG CCA GGC ACT TAC ATG
CTT ATG GAC GTG TGC GCT ACA AGG GAC GCT GAT GAT
AAA TGC ATC GAA GGC ACA ATT GTG GTG ACA GTC AGG
GTG TCC CTA TAT GAC GAA GAT AAC AAT GGT GTA ATG
GAT GAA GGT AAG GTG ATT CCA TCT GAG ACA ATC GAG
GAT GAT ATC AAG GAC TGT GGG CTC TTA GAC CAA GAT
GTT GAA CTC GAT TAT ACG TGG ACT CAA AAC GAG TGT
GAT CTA CCA GAC ACA GTA GAC GAG GCT GAA GAC ACA
CCG TCA GAA ACT GGA GAA TTC TTC TGG TAG
ATCTATCAGACTACTTTTATCAGCAGGACAACCTGGTCGTTACCAGAC
ACCTATAACGTGTCCTCATCAATAATGTGTAAAACAGAAATAATCGA
TAGAATATTGAAAATAAAATGTTAATAAACACTGGTTGAAATATGAA
AAAAAAAAAAAAAAAACTCGAG

Xho I

Fig. 4B

EEVQCAMNWTQANEYVFNVDMWTIFIYDYGAQEQLYEDRALGLCRIERAGPGTTKAV
WINWSNDTQSCVTRKTIFFEVGGEIARLVDRPQEDGTEKTFTTRKFSSKMPGTMYLM
DVCATRDADDKCIEGTIVVTVRVSLYDEDNNGVMDEGKVIPSETIEDDIKDCGLLDQ
DVELDYTWTQNECDLPDTVDEAEDTPSETGEFFW

Fig. 5A

MACIVFVALVALCLMQPGSGEEVQCAMNWTQANEYVFNVDMWTIFIYDYGAQEQLYE
DRALGLCRIERAGPGTTKAVWINWSNDTQSCVTRKTIFFEVGGEIARLVDRPQEDG
TEKTFTTRKFSSKMPGTMYLMDVCATRDADDKCIEGTIVVTVRVSLYDEDNNGVMDEG
KVIPSETIEDDIKDCGLLDQDVELDYTWTQNECDLPDTVDEAEDTPSETGEFFW

Fig. 5B

clone 40
BioXAct
rTth
GAATTCGGCACGAGTCGGAAAAGAACAAAATGGCTTGTATCGTTTTCGTT
TGGCTTGTATCGTTTTCGTT

clone 40
BioXAct
rTth
GCTCTTGTGCTCTATGCTTAATGCAACCGGGTTCCGGTGAGGAAGTACA
GCTCTTGTGCTCTATGCTTAATGCAACCGGGTTCCGGTGAGGAAGTACA
TATGCTTAATGCAACCGGGTTCCGGTGAGGAAGTACA

clone 40
BioXAct
rTth
ATGCGCGATGAATTGGACACAAGCTAATGAATATGTGTTCAACGTGGACT
ATGCGCGATGAATTGGACACAAGCTAATGAATATGTGTTCAACGTGGACT
ATGCGCGATGAATTGGACACAAGCTAATGAATATGTGTTCAACGTGGACT

clone 40
BioXAct
rTth
GGATGACCATTTTCATCTACGACTATGGCGCTCAAGAGCAACTGTACGAA
GGATGACCATTTTCATCTACGACTATGGCGCTCAAGAGCAACTGTACGAA
GGATGACCATTTTCATCTACGACTATGGCGCTCAAGAGCAACTGTACGAA

clone 40
BioXAct
rTth
GATCGGGCTTTGGGGCTGTGTGCGATTGAACGGGCCGGCCAGGTACCAC
GATCGGGCTTTGGGGCTGTGTGCGATTGAACGGGCCGGCCAGGTACCAC
GATCGGGCTTTGGGGCTGTGTGCGATTGAACGGGCCGGCCAGGTACCAC

clone 40
BioXAct
rTth
AAAAGCCGTCTGGATTAAGTGAAGTAACGACACGCGAGTCATGTGTAACAA
AAAAGCCGTCTGGATTAAGTGAAGTAACGACACGCGAGTCATGTGTAACAA
AAAAGCCGTCTGGATTAAGTGAAGTAACGACACGCGAGTCATGTGTAACAA

clone 40
BioXAct
rTth
GAAAAACAATCTTCTTCGAGGTTGGTGGAGAAATTGCCCGGCTAGTTGAC
GAAAAACAATCTTCTTCGAGGTTGGTGGAGAAATTGCCCGGCTAGTTGAC
GAAAAACAATCTTCTTCGAGGTTGGTGGAGAAATTGCCCGGCTAGTTGAC

clone 40
BioXAct
rTth
TACAGACCACAGGAAGACGGAAGTGAAGAACTTTTACAAGAAATTCTC
TACAGACCACAGGAAGACGGAAGTGAAGAACTTTTACAAGAAATTCTC
TACAGACCACAGGAAGACGGAAGTGAAGAACTTTTACAAGAAATTCTC

clone 40
BioXAct
rTth
TAGCAAAATGCCAGGCACTTACATGCTTATGGACGTGTGCGCTACAAGGG
TAGCAAAATGCCAGGCACTTACATGCTTATGGACGTGTGCGCTACAAGGG
TAGCAAAATGCCAGGCACTTACATGCTTATGGACGTGTGCGCTACAAGGG

clone 40
BioXAct
rTth
ACGCTGATGATAAATGCATCGAAGGCACAATTGTGGTGACAGTCAGGGTG
ACGCTGATGATAAATGCATCGAAGGCACAATTGTGGTGACAGTCAGGGTG
ACGCTGATGATAAATGCATCGAAGGCACAATTGTGGTGACAGTCAGGGTG

clone 40
BioXAct
rTth
TCCCTATATGACGAAGATAACAATGGTGTAAATGGATGAAGTAAGGTGAT
TCCCTATATGACGAAGATAACAATGGTGTAAATGGATGAAGTAAGGTGAT
TCCCTATATGACGAAGATAACAATGGTGTAAATGGATGAAGTAAGGTGAT

clone 40
BioXAct
TCCATCTGAGACAATCGAGGATGATATCAAGGACTGTGGGCTCTTAGACC
TCCATCTGAGACAATCGAGGATGATATCAAGGACTGTGGGCTCTTAGACC

Fig. 6 (Part 1 of 2)

09831142-050701
T02050-24TTES0

rTth	TCCATCTGAGACAATCGAGGATGATATCAAGGACTGTGGGCTCTTAGACC *****
clone 40	AAGATGTTGAACTCGATTATACGTGGACTCAAAACGAGTGTGATCTACCA
BioXAct	AAGATGTTGAACTCGATTATACGTGGACTCAAAACGAGTGTGATCTACCA
rTth	AAGATGTTGAACTCGATTATACGTGGACTCAAAACGAGTGTGATCTACCA *****
clone 40	GACACAGTAGACGAGGCTGAAGACACACCGTCAGAACTGGAGAATTCTT
BioXAct	GACACAGTAGACGAGGCTGAAGACACACCGTCAGAACTGGAGAATTCTT
rTth	GACACAGTAGACGAGGCTGAAGACACACCGTCAGAACTGGAGAATTCTT *****
clone 40	CTGGTAGATCTATCAGACTACTTTTATCAGCAGGACAACCTGGTCGTTACC
BioXAct	CTGGTAGATCTATCAGACTACTTTTATCAGCAGGACAACCTGGTCGTTACC
rTth	CTGGTANATCTATCAGACTACTTTTATCAGCAGGACAACCTGGTCGTTACC *****
clone 40	AGACACCTATAACGTGTCCTCATCAATAATGTGTAAACAGAAATAATCG
BioXAct	AGACACCTATAACGTGTCCTCATCAATAATGTGTAAACAGAAATAATCG
rTth	AGACACCTATAACGTGTCCTCATCAATAATGTGTAAAC *****
clone 40	ATAGAATATTGAAAATAAAATGTTAATAAACACTGGTTGAAATATGAAA
BioXAct	ATAGAATATTGAAAATAAAATGTTAATAAACACTGGTTGAAATATGAA
rTth	
clone 40	AAAAAAAAAAAAAACTCGAG
BioXAct	
rTth	

Fig. 6 (Part 2 of 2)

Oligo 1

ACI ATH TTY TTY CAR GT

Oligo 2

CAR GAR GAR GGN ACI GA

Oligo 2A

TCI GTN CCY TCY TCY TG

Oligo N

TTY AAY GTI GAY TGG ATG

M=A/C

R=A/G

W=A/T

S=G/C

Y=C/T

K=G/T

V=A/C/G

H=A/C/T

D=A/G/T

B=C/G/T

N=A/C/G/T

I=inosine

Fig. 7A

Oligo 3A

ACA CAG CCC CAA AGC CCG AT

Oligo 4S

.TTG CCC GGC TAG TTG ACT AC

Oligo 5A

CAT ATT TCA ACC AGT GTT TAT TAA

Oligo 6A

CAA TTG TGC CTT CGA TGC A

Oligo 7S

GGA CTG TGG GCT CTT AG

Oligo 8S

ATG GCT TGT ATC GTT TTC GT

Oligo T7

Fig. 7B

Oligo ExS

CCA CAC GGA TCC TGA GGA AGT ACA ATG

Oligo ExA

CCA CAC GGA TCC TTA TTG ATG AGG ACA

Oligo Bac1

CTT GTT TTT ATG GTC GTC TAC ATT TCT TAC ATC TAT GCG GAG
GAA GTA CAA TG

Oligo C9 12

CCA CAC AGA TCT AGA ATG AAA TTC TTA GTC AAC GTT GCC CTT
GTT TTT ATG GTC

Oligo BV5

TTT ACT GTT TTC GTA ACA GTT TTG

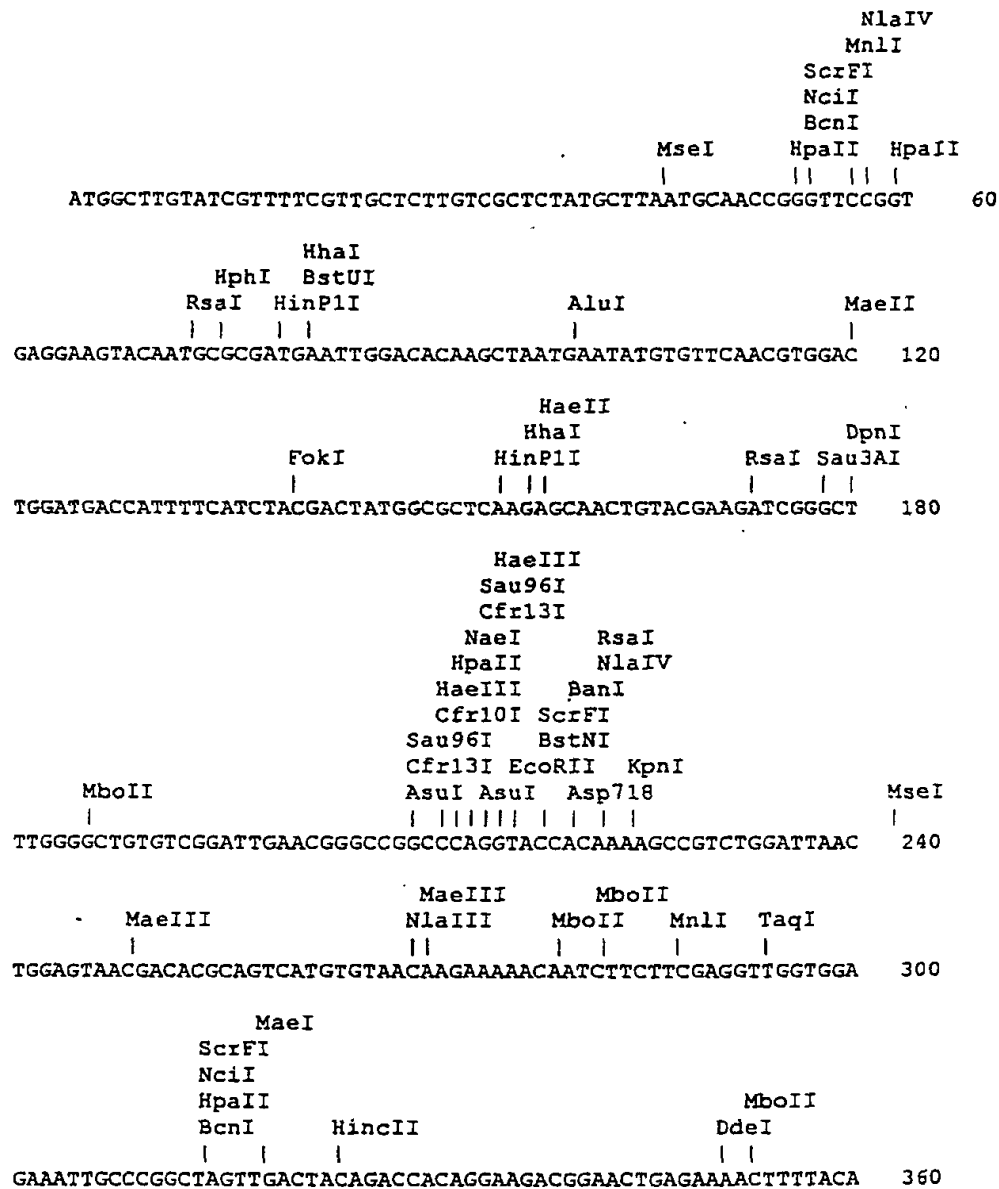
Oligo BV3

CAA CAA CGC ACA GAA TCT AG

Fig. 7C

AccI		630				
AflIII		405		734		
AluI 95						
AlwNI	659					
Asp 718		215				
AsuI		204	209			
BanI		215				
BanII		564				
BcnI		51	310			
BglII		678				
BspI 286		564				
BstNI		213		384		
BstUI	77					
CfrI10I	206					
CfrI13I	204		209			
DdeI		345		528		565
DpnI		174		615		680
EcoRI	665					
EcoRII	211		382			
EcoRV	547					
FokI		136		518		554
HaeII		153				
HaeIII	206		210			
HgaI		431				
HhaI		77		152		413
HincII		319				
HinfI		520		598		
HinPII	75		150		411	
HpaII	50		57		207	310
HphI	71		469		529	
KpnI		219				
MaeI		314		372		
MaeII		114		405	593	734
MaeIII	245		265		457	716
MboII	182		274		277	347
	497	653	661			
MnlI		54	282		531	627
	750					
MseI	41		237			
NaeI	208					
NciI		51		310		
NlaIII	264	397				
NlaIV	55		217			
NsiI		440				
NspHI	397					
PleI	592					
RsaI	69		167		217	
Sau3AI	172	613	678			
Sau96I	204	209				
ScrFI	51	213	310	384		
SfaNI	428					
TaqI 288		441	537	585		
XhoII		678				

Fig. 8

*Fig. 9 (Part 1 of 2)*

ScrFI
 BstNI
 MaeI EcoRII NspHI MaeII HinPII
 NlaIII AflIII HhaI
 AGAAAATTCTCTAGCAAAATGCCAGGCACCTTACATGCTTATGGACGTGTGCGCTACAAGG 420
 HgaI TaqI
 SfaNI NsiI MaeIII HphI
 GACGCTGATGATAAATGCATCGAAGGCACAATTGTGGTGACAGTCAGGGTGTCCTTATAT 480
 MnlI
 HinfI HphI
 MboII FokI DdeI TaqI
 GACGAAGATAACAATGGTGTAAATGGATGAAGGTAAGGTGATTCCATCTGAGACAATCGAG 540
 DdeI
 Bsp1286
 EcoRV FokI BanII TaqI MaeII
 PleI HinfI
 GATGATATCAAGGACTGTGGGCTCTTAGACCAAGATGTTGAACTCGATTATACGTGGACT 600
 DpnI AccI
 Sau3AI MnlI MboII AlwNI
 CAAAACGAGTGTGATCTACCAGACACAGTAGACGAGGCTGAAGACACACCGTCAGAACT 660
 DpnI
 XhoII
 EcoRI Sau3AI
 MboII BglII MaeIII
 GGAGAATTCTTCTGGTAGATCTATCAGACTACTTTTATCAGCAGGACAACCTGGTCGTTAC 720
 MaeII
 AflIII MnlI
 CAGACACCTATAACGTGTCCTCATCAATAA 750

Fig. 9 (Part 2 of 2)

